

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 15:22:32 ; Search time 182 Seconds
(without alignments)
7998.001 Million cell updates/sec

Title: US-09-989-862-284
Perfect score: 2623
Sequence: 1 ttgagcgacggtgagctctct.....taaaaaaaaaaaaaaaaaa 2623

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1113.6	42.5	1621	2	US-09-014-969-18
2	443.4	16.9	482	4	US-09-621-976-53
3	300.6	11.5	2330	4	US-09-800-729-12
4	108.4	4.1	3486	4	US-09-438-906-1
5	108.4	4.1	3486	4	US-09-438-906-3
6	54.2	2.1	1438	3	US-09-187-331-4
7	54.2	2.1	1438	4	US-09-470-946-4
8	54.2	2.1	3104	1	US-08-346-455B-66
9	54.2	2.1	3104	3	US-08-977-221-65
10	54.2	2.1	3104	5	US-09-483-831B-66
11	54.2	2.1	3104	5	PCT-US95-06613-35
12	53.4	2.0	3001	4	US-09-539-333D-215
13	53.3	2.0	90541	4	US-09-759-359A-3
14	52.4	2.0	3000	1	US-08-393-985-3
15	51.2	1.9	26000	4	US-09-843-376-10
16	51.1	1.9	2712	1	US-08-346-455B-37
17	51.1	1.9	2712	3	US-08-977-221-37
18	51.1	1.9	2712	4	US-09-483-831B-37
19	51.1	1.9	2712	5	PCT-US95-06613-37
20	51.1	1.9	2946	3	US-08-346-455B-35
21	51.1	1.9	2946	3	US-08-977-221-35
22	51.1	1.9	2946	4	US-09-483-831B-35
23	51.1	1.9	2946	5	PCT-US95-06613-35
24	51.1	1.9	3251	1	US-08-346-455B-68
25	51.1	1.9	3251	3	US-08-977-221-68
26	51.1	1.9	3251	4	US-09-483-831B-68
27	51.1	1.9	3251	5	PCT-US95-06613-68

28	51	1.9	6350	2	US-08-385-335A-9	Sequence 9, Appl1
29	50.6	1.9	4771	2	US-08-866-650-2	Sequence 2, Appl1
30	50.6	1.9	4771	2	US-09-021-287-2	Sequence 2, Appl1
31	50.6	1.9	4771	3	US-09-240-473-2	Sequence 2, Appl1
32	50.4	1.9	264	1	US-08-222-177A-10	Sequence 10, Appl1
33	50	1.9	11049	4	US-10-204-708-23	Sequence 23, Appl1
34	49.4	1.9	2614	4	US-09-052-753B-8	Sequence 1, Appl1
35	49	1.9	3474	4	US-09-527-236A-1	Sequence 1, Appl1
36	49	1.9	3474	4	US-09-756-854-1	Sequence 1, Appl1
37	48.6	1.9	1016	1	US-08-109-391A-3	Sequence 3, Appl1
38	48.6	1.9	1016	1	US-08-459-019A-3	Sequence 3, Appl1
39	48.6	1.9	1016	2	US-08-459-019A-3	Sequence 3, Appl1
40	48.6	1.9	1016	3	US-08-458-860A-3	Sequence 3, Appl1
41	48.6	1.9	51259	3	US-08-781-891-209	Sequence 209, App
42	48.6	1.9	51259	4	US-09-618-166-209	Sequence 209, App
43	48.4	1.8	324	1	US-08-222-177A-36	Sequence 36, Appl1
44	48.4	1.8	1936	4	US-09-566-921-41	Sequence 41, Appl1
45	48.4	1.8	8387	2	US-08-532-814-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-014-969-18
Sequence 18, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John W.
APPLICANT: Lavallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Apostolito, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-014-969-18
Query Match 42.5%; Score 1113.6; DB 2; Length 1621;
Best Local Similarity 94.7%; Pred. No. 4.4e-298;
Matches 1188; Conservative 0; Mismatches 4; Indels 62; Gaps 1;

QY 1 TTGACGCGAGGTGAGCTCTGAGGAGTTCGAGGAGGCTTCCTCCAGTACCCCTCCGCGGT 60
 Db 14 TTGACGCGAGGTGAGCTCTGAGGAGTTCGAGGAGGCTTCCTCCAGTACCCCTCCGCGGT 73
 QY 61 TACCGGCGGCGCGCGGAGGAGTCTCTCCAGACCTCCCTCCGCTGCTCCAACTAA 120
 Db 74 TACCGGCGGCGCGCGGAGGAGTCTCTCCAGACCTCCCTCCGCTGCTCCAACTAA 133
 QY 121 TACGAGCTGACCGAGTCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 Db 134 TACGAGCTGACCGAGTCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 158
 QY 181 AAGGCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240
 Db 159 -----GATTATCTTCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 191
 QY 241 AAATGACTTGGAAATTTATCTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 Db 192 AAATGACTTGGAAATTTATCTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 251
 QY 301 AACTTTCTCTCCAGCTGACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 Db 252 AACTTTCTCTCCAGCTGACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 311
 QY 361 TGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 Db 312 TGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 371
 QY 421 CAGGTGAAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
 Db 372 CAGGTGAAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 431
 QY 481 GTAACTGGCTCTTTCAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 Db 432 GTAACTGGCTCTTTCAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 491
 QY 541 CGGAACAAATCTTCTCCGCTGAGTCAATGAATTAATTAATTAATTAATTAATTA 600
 Db 492 CGGAACAAATCTTCTCCGCTGAGTCAATGAATTAATTAATTAATTAATTAATTA 551
 QY 601 GCGACACCAATATGATGATCAAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 Db 552 GCGACACCAATATGATGATCAAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 611
 QY 661 CCGGGAACAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720
 Db 612 CCGGGAACAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 671
 QY 721 TCAATTCATTTGAATGAGTTCGCAAAATTTGTAATGTTTGAATGTTTGAATGTT 780
 Db 672 TCAATTCATTTGAATGAGTTCGCAAAATTTGTAATGTTTGAATGTTTGAATGTT 731
 QY 781 AATAATCTTGGTCTTCTATTTGGGAGAGCCCTGATGACATGAGGAGGAGGAGGAG 840
 Db 732 AATAATCTTGGTCTTCTATTTGGGAGAGCCCTGATGACATGAGGAGGAGGAGGAG 791
 QY 841 GACGCTCGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 Db 792 GACGCTCGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 851
 QY 901 CAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 Db 852 CAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 911
 QY 961 GGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
 Db 912 GGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 971
 QY 1021 CACTATACCTGATGATCAATCTCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 Db 972 CACTATACCTGATGATCAATCTCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 1031

QY 1081 GATGAGCTGATGAGAGCTAATCTGAGCTGATCTTAACTTACTGTTTCAAAAAAGA 1140
 Db 1032 GATGAGGATTTAGAGAGCTAATCTGAGCTGATCTTAACTTACTGTTTCAAAAAAGA 1091
 QY 1141 GAGGTTCCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
 Db 1092 GAGGTTCCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1151
 QY 1201 GCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1254
 Db 1152 GCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1205
 RESULT 2
 US-09-621-976-53
 ; Sequence 53, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Meline Edwards, J.B.
 ; APPLICANT: Uobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.05492
 ; CURRENT APPLICATION NUMBER: US/09/621.976
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 53
 ; LENGTH: 482
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 74..481
 ; NAME/KEY: sig peptide
 ; LOCATION: 74..139
 ; OTHER INFORMATION: Von Heijne matrix
 ; OTHER INFORMATION: score 9
 ; OTHER INFORMATION: seq FILAUSLSTPS/LQ
 US-09-621-976-53
 Query Match 16 9%; Score 443.4; DB 4; Length 482;
 Best Local Similarity 99.8%; Pred. No. 7e-113;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 208 GATTAATCTTACAGTGAATGATCAAGTGAATTAATTAATTAATTAATTAATTAAT 267
 Db 38 GATTAATCTTACAGTGAATGATCAAGTGAATTAATTAATTAATTAATTAATTAAT 97
 QY 268 TCCCTCATCTTGGTCACTGAGTCTTTCACACCTTTTCTTCCAACTGAGACAGAA 327
 Db 98 TCCCTCATCTTGGTCACTGAGTCTTTCACACCTTTTCTTCCAACTGAGACAGAA 157
 QY 328 AAGGTTCAAGTCTTCTTGAAGGATTCGCTGAGGAGTCAATTAATTAATTAATTA 387
 Db 158 AAGGTTCAAGTCTTCTTGAAGGATTCGCTGAGGAGTCAATTAATTAATTAATTA 217
 QY 388 CCCCATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 447
 Db 218 CCCCATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 277
 QY 448 ATTAAACCAACCTTACCTTAACTTAATTAATTAATTAATTAATTAATTAATTAAT 507
 Db 278 ATTAAACCAACCTTACCTTAACTTAATTAATTAATTAATTAATTAATTAATTAAT 337
 QY 508 GGGATTTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 567
 Db 338 GGGATTTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 397
 QY 568 AAGAAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 627
 Db 398 AAGAAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 457

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 20, 2004, 20:34:08 ; Search time 105 Seconds

(without alignments)
2521.063 Million cell updates/sec

Title: US-09-989-862-285

Perfect score: 2561
Sequence: 1 WTSKFIIVSFIILALSIST.....SQTALQMAEIAQPLLOA 477

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xli
-G/cgn2 1/USPTO.spool/US09989862.rnmat 19042004.120333.8715/app.query.fasta_1.647
-DB-Issued Patents NA -GEMT-fastap -SUFFIX=cmi -NIMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=trans40.cdi
-LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09989862 @CGN 1.1.56 @rmat 19042004.120333.8715 -NCP=6 -ICPU=3
-NO MAP -LARGEJITTER -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /cgn2 6/ptodata/2/ina/5A COMB.seq:*
2: /cgn2 6/ptodata/2/ina/6A COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6B COMB.seq:*
4: /cgn2 6/ptodata/2/ina/6B COMB.seq:*
5: /cgn2 6/ptodata/2/ina/PTCUS COMB.seq:*
6: /cgn2 6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1810	70.7	1621	2	US-09-014-969-18
2	1034	40.4	2330	4	US-09-800-729-12
3	719	28.1	482	4	US-09-621-976-53
4	629.5	24.6	3486	4	US-09-438-906-1
5	629.5	24.6	3486	4	US-09-438-906-3
6	534.5	20.9	1438	3	US-09-187-331-4
7	534.5	20.9	1438	4	US-09-470-946-4
8	515.5	20.1	2586	4	US-09-221-017B-448
9	474.5	18.5	2946	1	US-08-346-455B-35
10	474.5	18.5	2946	3	US-08-977-221-35
11	474.5	18.5	2946	4	US-09-483-831B-35
12	474.5	18.5	2946	5	PCT-US95-06613-35

13	474.5	18.5	3251	1	US-08-346-455B-68	Sequence 68, Appl
14	474.5	18.5	3251	3	US-08-977-221-68	Sequence 68, Appl
15	474.5	18.5	3251	4	US-09-483-831B-68	Sequence 68, Appl
16	474.5	18.5	3251	5	PCT-US95-06613-68	Sequence 68, Appl
17	454	17.7	3104	1	US-08-346-455B-66	Sequence 66, Appl
18	454	17.7	3104	3	US-08-977-221-66	Sequence 66, Appl
19	454	17.7	3104	4	US-09-483-831B-66	Sequence 66, Appl
20	454	17.7	3104	5	PCT-US95-06613-66	Sequence 66, Appl
21	366.5	14.3	2712	1	US-08-346-455B-37	Sequence 37, Appl
22	366.5	14.3	2712	3	US-08-977-221-37	Sequence 37, Appl
23	366.5	14.3	2712	4	US-09-483-831B-37	Sequence 37, Appl
24	366.5	14.3	2712	5	PCT-US95-06613-37	Sequence 37, Appl
25	197	7.7	506	4	US-09-621-976-31	Sequence 31, Appl
26	181.5	7.1	486	4	US-09-621-976-3282	Sequence 3282, Ap
27	111.5	4.4	1770	4	US-09-543-681A-22	Sequence 22, Appl
28	107.5	4.2	3111	4	US-09-221-017B-922	Sequence 11, Appl
29	105.5	4.1	2531	4	US-09-468-656A-11	Sequence 11, Appl
30	103.5	4.0	1749	1	US-07-649-591B-2	Sequence 2, Appl
31	103.5	4.0	1749	1	US-08-277-540-2	Sequence 2, Appl
32	103.5	4.0	1749	1	US-08-430-787A-2	Sequence 2, Appl
33	103.5	4.0	2472	3	US-08-335-844A-7	Sequence 7, Appl
34	103.5	4.0	2472	4	US-09-129-366-7	Sequence 7, Appl
35	103.5	4.0	3358	3	US-08-335-844A-20	Sequence 20, Appl
36	103.5	4.0	3358	4	US-09-129-366-20	Sequence 20, Appl
37	102.5	4.0	1480	4	US-09-124-864-11	Sequence 11, Appl
38	102.5	4.0	359	4	US-08-561-527-243	Sequence 243, Appl
39	102	4.0	1545	1	US-07-621-670-1	Sequence 1, Appl
40	101	3.9	1625	4	US-09-813-133A-1	Sequence 1, Appl
41	101	3.9	1884	4	US-09-328-352-3421	Sequence 3421, Ap
42	99.5	3.9	2750	4	US-09-576-594-376	Sequence 376, Appl
43	99	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appl
44	99	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl
45	98.5	3.8	2290	3	US-08-961-083-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-014-969-18
Sequence 18, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: McCoy, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Metberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES
TITLE OR INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1621 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-014-969-18

Alignment Scores:

Pred. No.:	8,71e-211	Length:	1621
Score:	1810.00	Matches:	335
Percent Similarity:	99.41%	Conservative:	0
Best Local Similarity:	99.41%	Mismatches:	2
Query Match:	70.68%	Indels:	0
DB:	2	Gaps:	0

US-09-989-862-285 (1-477) x US-09-014-969-18 (1-1621)

QY 1 MetThrSerIysPheIleuValSerPheIleuValalaIleuSerLeuSerThrThr 20
 DB 195 ATGACTTCGAAATTTATCTGGTGTCCCTCATCTGTCGACAGTGGCTTTCAACAC 254
 QY 21 PheSerLeuGlnLeuSpGlnGlnIlyValLeuValSerPheSpGlyPheArgTTP 40
 DB 255 TTTTCTCTCCCAACCAACCAACCAAGGTTCTAGTTCTTTTGATGATTCGGTTGG 314
 QY 41 AspTyrLeuTyrIysValIProThProHisPheHisTyrIleMetIlyTyrGlyValHis 60
 DB 315 GATTACTTATATTAAGTCCAAAGCCCATTTCAATTATATTAAGAAATATGAGTTCAC 374
 QY 61 ValIysGlnValThrAsnValPheIleThrIysThrIyProAsnHisTyrThrIleuVal 80
 DB 375 GTGAAGCAAGTACTATATGTTTATTAACAAAACCTACCTAACCTATATCTTGGTA 434
 QY 81 ThrGlyLeuPhealagIusnHisGlyIleValAlaAsnSpMetPheAspProIleArg 100
 DB 435 ACTGGCTCTTGGACAGATCATGGATGTTGCAAAAGATATGTTGATCTCATTCGG 494
 QY 101 AsnIysSerPheSerLeuAspHisMetAsnIleTyrAspSerIysPheTTPGlnGlnAla 120
 DB 495 AACAAATCTTCTCTGGATCAACATGAATATTTAATGATTCAGTTTGGAGAGACG 554
 QY 121 ThrProIleTPIleThrAsnGlnArgAlaGlyHisThrSerGlyAlaAlaMetTTPPro 140
 DB 555 AACCCATATGATGATCAACCAACAGGCGGACGACATACATAGTGGACGACATGGGCC 614
 QY 141 GlyThrAspValIysIleHisIysArgPheProThHisTyrMetProTyrAsnGlnSer 160
 DB 615 GGAACAGATGTAATAATACATTAAGCGCTTCTCATCATTAACATGCTTCATCAATGAC 674
 QY 161 ValSerPheGluAspArgValAlaIysIleValGlnTTPPheThrSerIysGlnupProIle 180
 DB 675 GTTCAATTGAAGATGAAGTGCAGAAATGTTGAATGTTTACGTCAGAAAGGCCCA 734
 QY 181 AsnLeuGlyLeuLeuTyrTTPGlnAspProAspMetGlyHisHisIleuGlyProAsp 200
 DB 735 AATCTTGGTCTTCTCATTTGGGAAACCTCATATACATGGGCAACATTTGGGACCTGAC 794
 QY 201 SerProLeuMetGlyProValIleSerAspIleAspIlyLeuGlyTyrLeuIleGln 220
 DB 795 AGTCGCTCATGGGGCTGTCATTTCAATTTGACAGAAAGTTGAGATTCATCAACAA 854
 QY 221 MetLeuIysIysAlaIysLeuTTPAsnThrIleuAsnLeuIleIleThrSerAspHisGly 240
 DB 855 ATGCGAAGAAAGCGAAAGTTGTGAACCTGTGAACCTATATCAACAGATGATGGA 914
 QY 241 MetThrGlnCysSerGlnGlnArgLeuIleGlnLeuAspGlnIlyTyrLeuAspIysAspHis 260
 DB 915 ATGAGCGAGTCTCTGAGAAAGGTTAATATTAACCTTGAACATGATCTTGATTAAGACAC 974

QY 261 TyrThrIleuIleAspGlnSerProValAlaIleLeuProIysGlnGlyIysPheAsp 280
 DB 975 TATACCCGATGATATCAATTCAGATGACAGCCATCTTGGCAAGGATTAATTTAT 1034
 QY 281 GluValTyrGlnIleuThrHisAlaHisProAsnLeuThrValTyrIlySgIuAsp 300
 DB 1035 GAAGTTATGAAGCATTAACCTACGCTCATCTTACCTTACCTTACCTTACCTTACCT 1094
 QY 301 ValProGluArgTTPHisIlyTyrIysTyrAsnSerArgIleGlnProIleIleAlaValAla 320
 DB 1095 GTTCAGAAAGTGGCATTAACAAATTAACACATGCAATTAACCAATCAATCAATGAGCT 1154
 QY 321 AspGlnGlyTTPHisIleLeuGlnAsnIysSerAspAspPheLeuGly 337
 DB 1155 GATGAAGGATGGACATTTTACATTAAGATTAAGATGATGATGATGATGATGATG 1205

RESULT 2

US-09-800-729-12

Sequence 12, Application US/09800729

Patent No. 6605592

GENERAL INFORMATION:

APPLICANT: NI et al.

TITLE OF INVENTION: 32 Human secreted proteins

FILE REFERENCE: P2044P1

CURRENT APPLICATION NUMBER: US/09/800,729

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: PCT/US00/26013

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 12

LENGTH: 2330

TYPE: DNA

ORGANISM: Homo sapiens

US-09-800-729-12

Alignment Scores:

Pred. No.:	9,81e-116	Length:	2330
Score:	1034.00	Matches:	208
Percent Similarity:	62.03%	Conservative:	73
Best Local Similarity:	45.92%	Mismatches:	132
Query Match:	40.37%	Indels:	40
DB:	4	Gaps:	10

US-09-989-862-285 (1-477) x US-09-800-729-12 (1-2330)

QY 6 IleLeuValSerPheIleuAlaIleuSerLeuSerThrThrPheSerLeuGlnLeu 25
 DB 265 CTTATATTTTGGACATTTATTAACCTGTTGTGAGGTAACTTCCATAGCTG----- 318
 QY 26 AspGlnGlyValIleuValSerPheAspGlyPheArgTyrAspTyrLeuTyrIys 45
 DB 319 ----CATCCAGCTGCTGCGTGTGCTTTCATGCTTTCAGAGCGATCATTCACAAAG 375
 QY 46 ValProThProHisPheHisTyrIleMetIysTyrGlyValHisValIysGlnValThr 65
 DB 376 TATGAATTCCTCATCTCCAGATTTTATCAAGAGAGGCTCTGTGAGACAGATTAA 435
 QY 66 AsnValPheIleThrIysThrTyrProAsnHisTyrThrLeuValThrGlyLeuPheAla 85
 DB 436 AATGTTTTATCAAAACATTTCTTAACATCACTACAGATGATGACGGCTGTATGAA 495
 QY 86 GluAsnHisGlyIleValAlaAsnAspMetPheAspProIleArgAsnIysSerPheSer 105
 DB 496 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
 QY 106 LeuAspHisMetAsnIleTyrAspSerIys-----PheTyrGlnGlnAlaThrPro 122
 DB 547 -----CATTTTTCGACTTGTGATGACAAAGATCCTTTTGGTGAATGAGCGGATCT 600
 QY 123 IleTPIleThrAsnGln---ArgAlaGlyHisThrSerGlyAlaAlaMetTTPProGly 141

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 14:25:10 ; Search time 23 Seconds

(without alignments)
1070.678 Million cell updates/sec

Title: US-09-989-862-285

Perfect score: 2561
Sequence: 1 MTSKILVSLIAALSLSTT.....SQPLAQMAHIAQPLAQ 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodaca/2/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodaca/2/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodaca/2/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodaca/2/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodaca/2/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodaca/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1810	70.7	355	2	US-09-014-969-19
2	1034	40.4	453	4	US-09-800-729-83
3	719	28.1	136	4	US-09-621-976-3913
4	623.5	24.6	873	3	US-09-187-331-6
5	623.5	24.6	873	4	US-09-470-946-6
6	623.5	24.6	873	4	US-09-438-906-2
7	623.5	24.6	873	4	US-09-438-906-4
8	623.5	24.6	925	2	US-08-392-946-1
9	623.5	24.6	925	2	US-08-504-165-1
10	623.5	24.6	925	5	PCT-US94-14893-1
11	534.5	20.9	438	3	US-09-187-331-2
12	534.5	20.9	438	4	US-09-470-946-2
13	465.5	18.2	829	1	US-08-346-455B-34
14	465.5	18.2	829	3	US-08-977-221-33
15	465.5	18.2	829	4	US-09-483-831B-34
16	465.5	18.2	829	5	PCT-US95-06613-39
17	465.5	18.2	915	3	US-08-346-455B-69
18	465.5	18.2	915	3	US-08-977-221-69
19	465.5	18.2	915	4	US-09-483-831B-69
20	465.5	18.2	915	5	PCT-US95-06613-69
21	429.5	16.8	861	1	US-08-346-455B-67
22	429.5	16.8	861	1	US-08-977-221-67
23	429.5	16.8	861	4	US-09-483-831B-67
24	429.5	16.8	861	5	PCT-US95-06613-67
25	375	14.6	788	1	US-08-346-455B-36
26	375	14.6	788	3	US-08-977-221-36
27	375	14.6	788	4	US-09-483-831B-36

28	375	14.6	788	5	PCT-US95-06613-36	Sequence 36, Appl
29	371	14.5	979	1	US-08-346-455B-38	Sequence 38, Appl
30	371	14.5	979	3	US-08-977-221-38	Sequence 38, Appl
31	371	14.5	979	4	US-09-483-831B-70	Sequence 38, Appl
32	371	14.5	979	5	PCT-US95-06613-38	Sequence 38, Appl
33	197	7.7	151	4	US-09-621-976-3891	Sequence 3891, Ap
34	139.5	5.4	108	4	US-09-621-976-7142	Sequence 7142, Ap
35	111.5	4.4	589	4	US-09-543-681A-4194	Sequence 4194, Ap
36	109	4.3	709	4	US-09-668-673B-3	Sequence 3, Appl
37	105.5	4.1	819	4	US-09-468-656A-10	Sequence 10, Appl
38	101.5	4.0	972	3	US-08-335-844A-23	Sequence 23, Appl
39	101.5	4.0	972	4	US-09-129-366-23	Sequence 23, Appl
40	101	3.9	627	4	US-09-328-352-7547	Sequence 7547, Ap
41	98.5	3.8	763	3	US-08-961-083-66	Sequence 66, Appl
42	98.5	3.8	763	4	US-09-536-784-66	Sequence 66, Appl
43	98.5	3.8	838	4	US-09-468-656A-4	Sequence 4, Appl
44	98	3.8	1541	3	US-08-296-791-3	Sequence 3, Appl
45	98	3.8	1541	4	US-09-839-996-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-014-969-19
; Sequence 19, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Racine, Lisa A.
; APPLICANT: Metcalf, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Yakkil
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Springer, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-014-969-19
Query Match 70.7%; Score 1810; DB 2; Length 355;
Best Local Similarity 99.4%; Pred. No. 2.6e-173;
Matches 335; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY      1 MTSKFLVSLFLLAALSLSTFSLQDLOQKVLVSPDGRNDLYLKYPTPEHYIMKGYVH 60
DB      1 MTSKFLVSLFLLAALSLSTFSLQDLOQKVLVSPDGRNDLYLKYPTPEHYIMKGYVH 60
QY      61 VKQVTVVFITKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 120
DB      61 VKQVTVVFITKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 120
QY      121 TPWITNQRAGHTSGAAMPFGTDVYKHKRPETHYMEVSVSPEDRYAKIVEMFTSKPEPI 180
DB      121 TPWITNQRAGHTSGAAMPFGTDVYKHKRPETHYMEVSVSPEDRYAKIVEMFTSKPEPI 180
QY      181 NGLLIYMEDPDMDGHHILGPDSPIMGPVPSIDIKKGLYLIOMLKAKXIMNTLNIITSDHG 240
DB      181 NGLLIYMEDPDMDGHHILGPDSPIMGPVPSIDIKKGLYLIOMLKAKXIMNTLNIITSDHG 240
QY      241 MPOGSEERLISLDQYLDKDHVTLIDOSPVAAILPKRGRDHYEALTHAHPLTYKKED 300
DB      241 MPOGSEERLISLDQYLDKDHVTLIDOSPVAAILPKRGRDHYEALTHAHPLTYKKED 300
QY      301 VPERMHHYKNSRIQPIIAVADSGWHILQNKSDDFLLG 337
DB      301 VPERMHHYKNSRIQPIIAVADSGWHILQNKSDDFLLG 337

```

RESULT 2

```

US-09-800-729-83
; Sequence 83, Application US/09800729
; Patent No. 6605532
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-83

```

Query Match 40.4%; Score 1034; DB 4; Length 453;

Best Local Similarity 45.9%; Pred. No. 3,7e-95;

Matches 208; Conservative 73; Mismatches 132; Indels 40; Gaps 10;

```

QY      6 1LVSFLAALSLSTFSLQDLOQKVLVSPDGRNDLYLKYPTPEHYIMKGYVH 65
DB      7 LIPSGLITCCGSSSHSL--PSKLLVSPDGRADLTQNYFPLQNFIKESGVLEHAK 63
QY      66 NVFETKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 122
DB      64 NVFETKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 118
QY      123 IWTINQ-RAGHTSGAAMPFGTDVYKHKRPETHYMEVSVSPEDRYAKIVEMFTSKPEPI 180
DB      119 IWTINQENRSSAAAMPFGTDVPIHNTPTPEHYIMKGYVH 178
QY      181 NGLLIYMEDPDMDGHHILGPDSPIMGPVPSIDIKKGLYLIOMLKAKXIMNTLNIITSDHG 240
DB      179 TPWITNQRAGHTSGAAMPFGTDVYKHKRPETHYMEVSVSPEDRYAKIVEMFTSKPEPI 180
QY      240 GMTQGSERLISLDQYLDKDHVTLIDOSPVAAILPKRGRDHYEALTHAHPLTYKKED 300
DB      239 GMTQGSERLISLDQYLDKDHVTLIDOSPVAAILPKRGRDHYEALTHAHPLTYKKED 297
QY      300 VPERMHHYKNSRIQPIIAVADSGWHILQNKSDDFLLG 337

```

```

DB      298 DIPARFHYQANDRIQPIIAVADSGWHILQNKSDDFLLG 337
QY      360 RNFSEKMANSTDLVPLCHLNTTAMPHNGSSFWNVQDLNLSAMERVVPTOSTILLPGS 419
DB      357 HKQVTVVFITKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 120
QY      420 VKPNEYDQSGSYPTFGVSLGSIIVYFVFI 452
DB      408 -----IGIVGALVLTLLTCL 425

```

RESULT 3

```

US-09-621-976-3913
; Sequence 3913, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3913
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FRAGMENT:
; NAME/KEY: SIGNAL
; LOCATION: -22..-1
US-09-621-976-3913

```

Query Match 28.1%; Score 719; DB 4; Length 136;

Best Local Similarity 99.3%; Pred. No. 2.4e-64;

Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 MTSKFLVSLFLLAALSLSTFSLQDLOQKVLVSPDGRNDLYLKYPTPEHYIMKGYVH 60
DB      1 MTSKFLVSLFLLAALSLSTFSLQDLOQKVLVSPDGRNDLYLKYPTPEHYIMKGYVH 60
QY      61 VKQVTVVFITKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 120
DB      61 VKQVTVVFITKYPTNHYTLVTLGLFAENHGIIVANDMDPIRNKSFSLDHMTYDSKWEBA 120
QY      121 TPWITNQRAGHTSGA 136
DB      121 TPWITNQRAGHTSGA 136

```

RESULT 4

```

US-09-187-331-6
; Sequence 6, Application US/09187331
; Patent No. 6043056
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Baughn, Marian R.
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
; FILE REFERENCE: PF-0631 US
; CURRENT APPLICATION NUMBER: US/09/187,331
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -

```